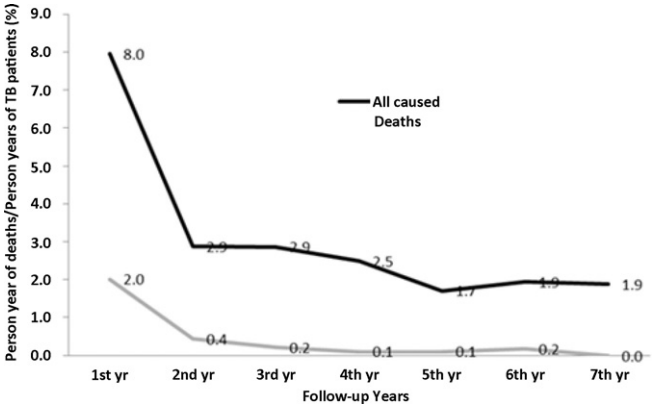

Figure 1. Total and TB specific deaths among TB patients during different follow-up years.

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Deaths of tuberculosis patients in urban China: a retrospective cohort study

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Background: The proportion of tuberculosis (TB) patients in China who die remains high (5%). The aim of the present study was to determine the factors associated with TB-cause or all-cause deaths among TB patients in urban China.

Methods: It was a retrospective cohort study among all pulmonary TB patients registered in the four districts during 2004 -2008 based on the China National TB Surveillance System. Finally 4,271 were successfully followed up in communities and included in analysis by cox regression.

Results: It was observed that the proportion of deaths by all possible causes for the TB patients was 15% after 2-6 years from recent TB diagnosis. Among the dyed patients, only 17% was directly caused by TB, and the remainder (83%) was due to one or more causes other than TB. Male sex was significantly associated with all caused deaths. After adjusting sex, age and treatment history, psychopathy, chronic bronchitis, cancer and multiple diseases were significantly associated with higher risk of death. Totally, TB was responsible for 7.2 PYLLs per case, with 5.3 in male and 8.2 in female patients.

Fig. 1.

Conclusion: Both TB control programs and other public health programs should be strengthened and interact with each other. These findings highlight the importance of improved clinical management and prevention strategies that target TB patients at increased risk of death.

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Detection of genomic mutations in katG, inhA and rpoB genes of *Mycobacterium tuberculosis* isolates using polymerase chain reaction and multiplex allele-specific polymerase chain reaction (MAS-PCR)

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Background: Isoniazid and Rifampin are the most effective first line antibiotics against *Mycobacterium tuberculosis.* Mutations in several genes are determining the resistance of *M. tuberculosis* to Isoniazid, with the most common gene target of KatG, and resistance to Rifampin is due to mutation in rpoB gene. The aim of present study was to determine the mutations in the regions related to Rifampin and Isoniazid resistance IN *M. tuberculosis* strains isolated from tuberculosis patients in Ahvaz, Iran.

Methods: We characterized 80 clinical isolates of confirmed *M. tuberculosis* to analyze the most commonly observed Isoniazid and Rifampin mutations. PCR analysis with subsequent sequencing were used to detect mutations related to Rifampin and Isoniazid resistance. The multiplex allele-specific-PCR, was performed as a comparative assay and for evaluation of this method.

Results: The sequencing of the 250-bp region of katG codon 315, revealed point mutations at 5 different codons in 13.7% of the *M. tuberculosis* isolates. The sequencing of the 270-bp central region of the rpoB gene, revealed point mutations at 7 different codons in 12 (15%) of the *M. tuberculosis* isolates. The results obtained with multiplex allele-specific-PCR assay, were in concordance to PCR-sequencing with high sensitivity and specificity for katG315, inhA15, and rpoB (531, 516, 526).

Conclusion: The result of this study suggested that molecular techniques can be used as a rapid tool for the identification of drug resistance in clinical isolates of *M. tuberculosis*. Both DNA sequencing and multiplex allele-specific -PCR technique gave a high value sensitivity for the detection of Rifampin and Isoniazid mutations and detecting multi-drug resistant tuberculosis cases.

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